

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Wei-Wu He, Kristine K. Kikly, Vishva M. Dixit, Steven M. Ruben

(ii) TITLE OF THE INVENTION: INTERLEUKIN-1 BETA CONVERTING ENZYME LIKE APOPTOSIS PROTEASE-6

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: SmithKline Beecham Corporation
- (B) STREET: 709 Swedeland Road
- (C) CITY: King of Prussia
- (D) STATE: PA
- (E) COUNTRY: USA
- (F) ZIP: 19406-2799

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: UNKNOWN
- (B) FILING DATE: HEREWITH
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 60/018,961
- (B) FILING DATE: 05 JUNE 1996

- (A) APPLICATION NUMBER: 60/020,344
- (B) FILING DATE: 23 MAY 1996

- (A) APPLICATION NUMBER: 60/017,949
- (B) FILING DATE: 20 May 1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Han, William T.
 (B) REGISTRATION NUMBER: 34,344
 (C) REFERENCE/DOCKET NUMBER: P50483-2

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 610-270-5219
 (B) TELEFAX: 610-270-5090
 (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 416 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

Met Asp Glu Ala Asp Arg Arg Leu Leu Arg Arg Cys Arg Leu Arg Leu
 1             5             10             15
Val Glu Glu Leu Gln Val Asp Gln Leu Trp Asp Val Leu Leu Ser Arg
 20             25             30
Glu Leu Phe Arg Pro His Met Ile Glu Asp Ile Gln Arg Ala Gly Ser
 35             40             45
Gly Ser Arg Arg Asp Gln Ala Arg Gln Leu Ile Ile Asp Leu Glu Thr
 50             55             60
Arg Gly Ser Gln Ala Leu Pro Leu Phe Ile Ser Cys Leu Glu Asp Thr
 65             70             75             80
Gly Gln Asp Met Leu Ala Ser Phe Leu Arg Thr Asn Arg Gln Ala Gly
 85             90             95
Lys Leu Ser Lys Pro Thr Leu Glu Asn Leu Thr Pro Val Val Leu Arg
100            105            110
Pro Glu Ile Arg Lys Pro Glu Val Leu Arg Pro Glu Thr Pro Arg Pro
115            120            125
Val Asp Ile Gly Ser Gly Gly Phe Gly Asp Val Gly Ala Leu Glu Ser
130            135            140

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Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys			
145	150	155	160
Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly			
	165	170	175
Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg			
	180	185	190
Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr			
	195	200	205
Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His			
	210	215	220
Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln			
	225	230	235
Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys			
	245	250	255
Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys			
	260	265	270
Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly			
	275	280	285
Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu			
	290	295	300
Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln			
	305	310	315
Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro			
	325	330	335
Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val			
	340	345	350
Ser Trp Arg Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp			
	355	360	365
Asp Ile Phe Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu			
	370	375	380
Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met			
	385	390	395
Pro Gly Cys Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser			
	405	410	415

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCCATGGACG	AAGCGGATCG	GCGGCTCCTG	CGGCGGTGCC	GGCTGCGGCT	GGTGAAGAG	60
CTGACGGTGG	ACACGCTCTG	GGACGTCCCTG	CTGAGCGCGG	AGCTGTTCAG	GCCCCATATG	120
ATCGAGGACA	TCCAGCGGGC	AGGCTCTGGA	TCTCGGCGGG	ATCAGGCCAG	GCAGCTGATC	180
ATAGATCTGG	AGACTCGAGG	GAGTCAGGCT	CTTCCTTTGT	TCATCTCCCTG	CTTAGAGGAC	240
ACAGGCGCAG	ACATGCTGGC	TTCTGTTTCTG	CGAACTAACA	GGCAAGCAGG	AAAGTTGTCTG	300
AAGCCCAACCC	TAGAAAACCT	TACCCAGATG	GTGCTCAGAC	CAGAGATTCTG	CAAACACAGAG	360
GTTCTCAGAC	CGGAAACACC	CAGACCAGTG	GACATTGGTT	CTGGAGGATT	CGGTGATGTC	420
GGTGCTCTTG	AGAGTTTGAG	GGGAAATGCA	GATTTGGCTT	ACATCCTGAG	CATGGAGCCC	480
TGTGGCCACT	GCCTCATTAT	CAACAATGTG	AACCTCTGCC	GTGAGTCCGG	GCTCCGCACC	540
CGCACTGGCT	CCAACATCGA	CTGTGAGAAG	TTGCGGCGCTC	GCTTCTCCTC	GCTGCATTTC	600
ATGGTGGAGG	TGAAGGGCGA	CCTGACTGCC	AAGAAAATGG	TGCTGGCTTT	GCTGGAGCTG	660
GCGGGCGCAG	ACCACGGTGC	TCTGGACTGC	TGCGTGGTGG	TCATTCTCTC	TCACGGCTGT	720
CAGGGCAGCC	ACCTGCAGTT	CCCAGGGGCT	GTCTACGGCA	CAGATGGATG	CCCTGTGTCTG	780
GTCGAGAAGA	TTGTGAACAT	CTTCAATGGG	ACCAGCTGCC	CCAGCTCTGGG	AGGGAAGCCC	840
AAGCTCTTTT	TCATCCAGGC	CTGTGGTGGG	GAGCAGAAAG	ACCATGGGTT	TGAGGTGGCC	900
TCCACTTCCC	CTGAAGACGA	GTCCCTTGCC	AGTAACCCCG	AGCCAGATGC	CACCCCGTTC	960
CAGGAAGGTT	TGAGGACCTT	CGACCAGCTG	GACGCCATAT	CTAGTTTGCC	CACAGCCAGT	1020
GACATCTTTG	TGTCTTACTC	TACTTTCCTA	GGTTTGTGTT	CCTGGAGGGA	CCCCAAGAGT	1080
GGCTCTTGTT	ACGTTGAGAC	CCTGGACGAC	ATCTTTGAGC	AGTGGGCTCA	CTCTGAAGAC	1140
CTGCAGTCCC	TCCTGCTTAG	GGTGCTTAAT	GCTGTTTCGG	TGAAAAGGGAT	TTATAAACAG	1200
ATGCTCTGTT	GCTTTAATTT	CCTCCGGAAG	AAACTTTTCT	TTAAAACATC	ATAAGGCCAG	1260
GGCCCCCTAC	CCTGCTTAT	CTTGACACCC	AAAGCTTTCC	TGCCCCAGGC	CTGAAAGAGG	1320
CTGAGGCGCT	GACTTTCTCTG	CAACTCAAGG	ACTTTGNAGC	CGGCACAGGG	TCTGCTCTTT	1380
CTCTGCCAGT	GACAGACAGG	CTCTTAGCAG	CTTCCAGATT	GACGACAAGT	GCTGAACAGT	1440
GGAGGAAGAG	GGACAGATGA	ATGCCGTGGA	TTGCACGTGG	NCTCTTGAGC	AGTGGCTGTT	1500
CCAGGGCTAG	TGACTTTGTTG	TCCCATGATC	CCTGTGTGG	TCTTAGGAG	CAGGGATTAA	1560
CCTCTGCACT	ACTGACAT					1578

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGACTGCCA AGAAAAATGGT GCTGGCTTTG CTGGAGCTGG CGGGGCAGGA CCACGGTGCT	60
CTGGACTGCT GCGTGCTGGT CATCTCTCT CACGGCTGTC AGGCCAGCCA CCTGCAGTTC	120
CCAGGGCGCTG TCTACGGCAC AGATGGATGC CCTGTGTCCG TCGAAAAGAT TGTGAACATC	180
TTCAATGGGA CCAGCTGCCC CAGCCTGGGA GGAAGGCCA AGCTCTTTT CATCCAGGCC	240
TGTGGTGGG AGCAGAAAGA CCATGGGTTT GAGGTGGCCT CCACCTCCCC TGAAGACGAG	300
TCCCCTGGCA GTAACCCCGA GCCAGATGCC ACCCCGTTC AGGAAGGTTT GAGGACCTTC	360
GACCAGCTGG ACGCCATATC TAGTTTGGCC ACACCCAGTG ACATCTTTGT GTCCTACTCT	420
ACTTTCCAG GTTTTGTTC CTGGAGGGAC CCGAAGAGTG GTCCTGGTA CGTTGAGACC	480
CTGGACGACA TCTTTGAGCA GTGGCTCAC TCTGAAGACC TGCAGTCCCT CCTGCTTAGG	540
GTCCGCTAATG CTGTTCGT GAAAGGATT TATAACAGA TGCGTGGTTG CTTTAATTTT	600
CTCCGAAAAA AACTTTTCTT TAAACATC ATAAGGCAG	639

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His Gly Ala Leu	
1 5 10 15	
Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln Ala Ser His	
20 25 30	
Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys Pro Val Ser	
35 40 45	
Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys Pro Ser Leu	
50 55 60	
Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly Gly Glu Gln	

65		70		75		80									
Lys	Asp	His	Gly	Phe	Glu	Val	Ala	Ser	Thr	Ser	Pro	Glu	Asp	Glu	Ser
				85					90					95	
Pro	Gly	Ser	Asn	Pro	Glu	Pro	Asp	Ala	Thr	Pro	Phe	Gln	Glu	Gly	Leu
			100					105					110		
Arg	Thr	Phe	Asp	Gln	Leu	Asp	Ala	Ile	Ser	Ser	Leu	Pro	Thr	Pro	Ser
		115				120					125				
Asp	Ile	Phe	Val	Ser	Tyr	Ser	Thr	Phe	Pro	Gly	Phe	Val	Ser	Trp	Arg
	130					135					140				
Asp	Pro	Lys	Ser	Gly	Ser	Trp	Tyr	Val	Glu	Thr	Leu	Asp	Asp	Ile	Phe
	145			150					155					160	
Glu	Gln	Trp	Ala	His	Ser	Glu	Asp	Leu	Gln	Ser	Leu	Leu	Leu	Arg	Val
			165					170						175	
Ala	Asn	Ala	Val	Ser	Val	Lys	Gly	Ile	Tyr	Lys	Gln	Met	Pro	Gly	Cys
			180					185					190		
Phe	Asn	Phe	Leu	Arg	Lys	Lys	Leu	Phe	Phe	Met					
		195					200								

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAACGGGGTA CCGCCATGGA CGAAGCGGAT CGGC

34

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGCTCTAGAT TAGTGGTGGT GGTGGTGGTG TGATGTTTAA AAGAAAAGTT TTTTCCGGAG 60

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGCTCTTTT TCATCCAGGC CGCGGGTGGG GAGCAGAAGA C 41

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCTTTCTGC TCCCCACCCG CGGCCTGGAT GAAAAAAGC

39

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGCTCTAGAT TACTGTGCAT CGTCGTCCTT GTAGTCTGAT GTTTTAAAGT TAAGTTTTTT	60
CCGGAG	66

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: DIXIT, VISHVA M.
HE, WEI-WU
KIKLY, KRISTINE K.
RUBEN, STEVEN M.
- (ii) TITLE OF THE INVENTION: INTERLEUKIN-1 BETA CONVERTING
ENZYME LIKE APOPTOTIC PROTEASE-6
- (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Ratner & Prestia
(B) STREET: P.O. Box 980
(C) CITY: Valley Forge
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19482
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/952,936
(B) FILING DATE: 08-MAY-1997
(C) CLASSIFICATION: UNKNOWN
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/013,961
(B) FILING DATE: 05-JUN-1996

(A) APPLICATION NUMBER: 60/020,344
(B) FILING DATE: 23-MAY-1996

(A) APPLICATION NUMBER: 60/017,949
(B) FILING DATE: 20-MAY-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Prestia, Paul F
(B) REGISTRATION NUMBER: 23,031
(C) REFERENCE/DOCKET NUMBER: p80483-2
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 610-407-0700
(B) TELEFAX: 610-407-0700
(C) TELEX: 346159
- (2) INFORMATION FOR SEQ ID NO:1:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

Met Asp Glu Ala Asp Arg Arg Leu Leu Arg Arg Cys Arg Leu Arg Leu
 1      5      10      15
Val Glu Glu Leu Gln Val Asp Gln Leu Trp Asp Val Leu Leu Ser Arg
 20      25      30
Glu Leu Phe Arg Pro His Met Ile Glu Asp Ile Gln Arg Ala Gly Ser
 35      40      45
Gly Ser Arg Arg Asp Gln Ala Arg Gln Leu Ile Ile Asp Leu Glu Thr
 50      55      60
Arg Gly Ser Gln Ala Leu Pro Leu Phe Ile Ser Cys Leu Glu Asp Thr
 65      70      75      80
Gly Gln Asp Met Leu Ala Ser Phe Leu Arg Thr Asn Arg Gln Ala Gly
 85      90      95
Lys Leu Ser Lys Pro Thr Leu Glu Asn Leu Thr Pro Val Val Leu Arg
100      105      110
Pro Glu Ile Arg Lys Pro Glu Val Leu Arg Pro Glu Thr Pro Arg Pro
115      120      125
Val Asp Ile Gly Ser Gly Gly Phe Gly Asp Val Gly Ala Leu Glu Ser
130      135      140
Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys
145      150      155      160
Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly
165      170      175
Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg
180      185      190
Arg Phe Ser Ser Leu His Phe Met Val Ile Val Lys Gly Asp Leu Thr
195      200      205
Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His
210      215      220
Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln
225      230      235      240
Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys
245      250      255
Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys
260      265      270
Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly
275      280      285
Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu
290      295      300
Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln
305      310      315      320
Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro
325      330      335
Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val
340      345      350
Ser Trp Arg Asp Pro Cys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp
355      360      365

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Asp	Ile	Phe	Glu	Gln	Trp	Ala	His	Ser	Glu	Asp	Leu	Gln	Ser	Leu	Leu
370						375					380				
Leu	Arg	Val	Ala	Asn	Ala	Val	Ser	Val	Lys	Gly	Ile	Tyr	Lys	Gln	Met
385				390						395				400	
Pro	Gly	Cys	Phe	Asn	Phe	Leu	Arg	Lys	Lys	Leu	Phe	Phe	Lys	Thr	Ser
			405					410					415		

(2) INFORMATION FOR SEQ ID NO:2:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCCATGAGAC	AAGCGGATCG	GCGGCTCCTG	CGGCGGTGCC	GGGTGGGGCT	GGTGGGAGAG	60
CTGCAGGTGG	ACCAGCTCTG	GGACGTCTCT	CTGAGCGCGG	AGCTGTTCAG	GCCTCATATG	120
ATCGAGGACA	TCCAGCGGGC	AGGCTCTGGA	TCTCGGCGGG	ATCAGGCCAG	CGACGTGATG	180
ATAGATCTGG	AGACTCGAGG	SAGTCAGGGT	CTTCTTTTGT	TGATCTCTTG	CTTAGAGGAC	240
ACAGGCGCAG	ACATGCTGGC	TTCGTTTCTG	CGAACTAAGA	GGCAGGCAGG	AAAGTTGTCT	300
AAGCCAAACG	TAGAAAACCT	TACCCAGATG	TGCTCAGAC	CAGAGATTCT	CAAAACGAGG	360
GTTCCTCAGC	CGGAAACACC	CAGACCGAGT	GACATTGGTT	CTGGAGGATT	CGGTGATGTC	420
GGTGCTCTTG	AGAGTTTGAG	GGGAAATGCA	GATTTTGGCT	ACATCTCTGAG	CATGGAGCCC	480
TGTGGCCACT	GCCTCATAT	CAACAATGTG	AACTTTTGCC	TGAGTTCGGG	GCTCCGACCC	540
CGCACTGGCT	CCACATCGA	CTGTGAGAAG	TGCGGCGGTC	GCTTCTCTCT	GCTGCATTTC	600
ATGGTGGAGG	TGAAGGGCGA	CCTGACTGCC	ARGAAAAATG	TGCTGGCTTT	GCTGGAGCTG	660
GCGCGGCAGG	ACCACGGTGC	TCTGACTGTC	TGCTGGTGGG	TGATCTCTCT	TGACGGCTGT	720
CAGGCGAGCC	ACCTGCAGTT	CCGAGGGGCT	GTCTACGGCA	CAGATGGATG	CCCTGTGTCT	780
GTGAGAGAAG	TGTGACAGAT	CTTCAATGGG	ACCAGCTGCC	CCAGCCTGGG	AGGGAAGCCC	840
AAGCTCTTTT	TGATCCAGGC	CTGTGGTGGG	SAGCAGAAAG	ACCATGGGTT	TGAGCTGGCC	900
TCCACTTCCC	CTGAGAGGCA	GTCCCTGTGG	AGTAAGCCCG	AGCCAGATGC	CACCCGCTTC	960
CAGGAAGGTT	TGAGGACCTT	CGACGAGCTG	SAGCGCATAT	TGAGTTTGGC	CACACCCAGT	1020
GACATCTCTG	TGCTCTACTC	TACTTTCCCA	GGTTTTGTTT	CTGGAGGGGA	CCCCCAAGAGT	1080
GGCTCTTGTT	ACGTTGAGAC	CTGGAGCAGC	ATCTTTGAGC	AGTGGGCTCA	CTCTGAAGAC	1140
CTGCAGTCCC	TCTTGCTTAG	GTGCTCTAAT	GCTGTTTCGG	TGAAGGGGAT	TTATTAACAG	1200
ATGCCGTGGT	GCTTTAATTT	CCTCCGGAAA	AAAGCTTTCT	TTAAAGCATC	ATAAGGCCAG	1260
GGCCCTCTAC	CCTGCCCTAT	CTTGACACCC	AAAGCTTTCC	TGCCCCAGGC	CTGAAGAGGG	1320
CTGAGGCGTG	GACTTTCTCT	CAACTCAAGG	ACTTTGNAGC	CGGCACAGGG	TCTGCTCTTT	1380
CTCTGCCAGT	GACAGACAGG	CTCTTAGCAG	CTTCCAGATT	GACGACAAGT	GCTGAACAGT	1440
GGAGGAAGAG	GGACAGATGA	ATGCCCTGGA	TGACAGCTGG	NCCTCTGAGC	AGTGGCTGGT	1500
CGAGGGCTAG	TGACTTGGTG	TCCCATGATC	CCTGTGTTTG	TCTCTAGGAG	CAGGGATTA	1560
CTCTGCACT	ACTGACAT					1578

(2) INFORMATION FOR SEQ ID NO:3:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGACTGCCA	AGAAATGGT	GCTGGCTTTG	CTGGAGCTGG	CGCGGCAGGA	CCACGGTGCT	60
CTGGACTGCT	GGGTGGTGGT	CATTCTCTCT	CACGGCTGTC	AGGCCAGCCA	CCTGCAGTTC	120
CCAGGGGCTG	TCTACGGCAC	AGATGGATGC	CCTGTSTCGG	TGAAAAAGAT	TGTGAACATC	180
TTCAATGGGA	CCAGCTGCCC	CAGCCTGGGA	GGGAAGCCCA	AGCTCTTTTT	CATCCAGGGC	240
TGTGGTGGGG	AGCAGAAAGA	CCATGGGTTT	GAGGTGGCT	CCACTTCCCC	TGAAGACGAC	300
TGCTTGGCA	GTAACCCCGA	CCAGATGCC	ACCCGCTTCC	AGGAAGGTTT	GAGGACCTTC	360
GACGAGCTGG	ACGGCATATC	TAGTTTGGCC	ACACCCAGTG	ACATCTTTGT	GTCTACTCT	420
ACTTTCCGAG	GTTTGTGTTT	CTGGAGGGAC	CCCAAGAGTG	GCTCCTGGTA	CGTTGAGACC	480
CTGGACGACA	TCTTTGAGCA	GTGGGCTCAC	TCTGAAGACC	TGCAGTCCCT	CCTGCTTAGG	540
GTGCTTAATG	CTGTTTCGGT	GAAAGGGATT	TATAAACAGA	TGCCTGGTTG	CTTTAATTTC	600
CTCCGAAAAA	AACTTTTCTT	TTAAACATC	ATAAGGCAG			639

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His Gly Ala Leu
1 5 10 15
Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln Ala Ser His
20 25 30
Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys Pro Val Ser
35 40 45
Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys Pro Ser Leu
50 55 60
Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly Gly Glu Gln
65 70 75 80
Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu Asp Glu Ser
85 90 95
Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln Glu Gly Leu
100 105 110
Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro Thr Pro Ser
115 120 125
Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val Ser Trp Arg
130 135 140
Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp Asp Ile Phe
145 150 155 160
Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu Leu Arg Val
165 170 175
Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met Pro Gly Cys
180 185 190
Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Met
195 200

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAACGGGGTA CGCCATGGA CGAAGCGGAT CGGC 34

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGCTCTAGAT TAGTGGTGT GGTGGTGGTG TGATGTTTAA AAGAAAAGTT TTTCCGGAG 60

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGCTCTTTT TCATCCAGGC CGCGGGTGGG GAGCAGAAGA C 41

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCTTCTGTC TCCGACCGG CGCGCTGGAT GAAAAAAGC 39

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGCTCTAGAT TACTTGTCAT CGTCTGCTT GTAGTCGTAT GTTTAAAGT TAAGTTTTTT
CCGGAG

60
66

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gln Ala Cys Arg Gly
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gln Ala Cys Gly Gly
1 5